

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Goodwin, Raymond G.
Smith, Craig A.
Armitage, Richard J.
Gruss, Hans-Jurgen
- (ii) TITLE OF INVENTION: Novel Cytokine That Binds CD30
- (iii) NUMBER OF SEQUENCES: 23
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Kathryn A. Seese, Immunex Corporation
 - (B) STREET: 51 University Street
 - (C) CITY: Seattle
 - (D) STATE: Washington
 - (E) COUNTRY: USA
 - (F) ZIP: 98101
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/225,989
 - (B) FILING DATE: 12-APR-1994
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/966,775
 - (B) FILING DATE: 27-OCT-1992
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 907,224
 - (B) FILING DATE: 01-JUL-1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 899,660
 - (B) FILING DATE: 15-JUN-1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 892,459
 - (B) FILING DATE: 02-JUN-1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 889,717
 - (B) FILING DATE: 26-MAY-1992
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Seese, Kathryn A.
 - (B) REGISTRATION NUMBER: 32,172
 - (C) REFERENCE/DOCKET NUMBER: 2804-E
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (206)587-0430

(B) TELEFAX: (206)233-0644
(C) TELEX: 756822

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1788 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: huCD30

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG	CGC	GTC	CTC	CTC	GCC	GCG	CTG	GGA	CTG	CTG	TTC	CTG	GGG	GCG	CTA	48
Met	Arg	Val	Leu	Leu	Ala	Ala	Leu	Gly	Leu	Leu	Phe	Leu	Gly	Ala	Leu	
1				5				10						15		
CGA	GCC	TTC	CCA	CAG	GAT	CGA	CCC	TTC	GAG	GAC	ACC	TGT	CAT	GGA	AAC	96
Arg	Ala	Phe	Pro	Gln	Asp	Arg	Pro	Phe	Glu	Asp	Thr	Cys	His	Gly	Asn	
			20					25					30			
CCC	AGC	CAC	TAC	TAT	GAC	AAG	GCT	GTC	AGG	AGG	TGC	TGT	TAC	CGC	TGC	144
Pro	Ser	His	Tyr	Tyr	Asp	Lys	Ala	Val	Arg	Arg	Cys	Cys	Tyr	Arg	Cys	
		35					40					45				
CCC	ATG	GGG	CTG	TTC	CCG	ACA	CAG	CAG	TGC	CCA	CAG	AGG	CCT	ACT	GAC	192
Pro	Met	Gly	Leu	Phe	Pro	Thr	Gln	Gln	Cys	Pro	Gln	Arg	Pro	Thr	Asp	
	50					55				60						
TGC	AGG	AAG	CAG	TGT	GAG	CCT	GAC	TAC	TAC	CTG	GAT	GAG	GCC	GAC	CGC	240
Cys	Arg	Lys	Gln	Cys	Glu	Pro	Asp	Tyr	Tyr	Leu	Asp	Glu	Ala	Asp	Arg	
65				70				75						80		
TGT	ACA	GCC	TGC	GTG	ACT	TGT	TCT	CGA	GAT	GAC	CTC	GTG	GAG	AAG	ACG	288
Cys	Thr	Ala	Cys	Val	Thr	Cys	Ser	Arg	Asp	Asp	Leu	Val	Glu	Lys	Thr	
			85					90						95		
CCG	TGT	GCA	TGG	AAC	TCC	TCC	CGT	GTC	TGC	GAA	TGT	CGA	CCC	GGC	ATG	336
Pro	Cys	Ala	Trp	Asn	Ser	Ser	Arg	Val	Cys	Glu	Cys	Arg	Pro	Gly	Met	
		100						105					110			
TTC	TGT	TCC	ACG	TCT	GCC	GTC	AAC	TCC	TGT	GCC	CGC	TGC	TTC	TTC	CAT	384
Phe	Cys	Ser	Thr	Ser	Ala	Val	Asn	Ser	Cys	Ala	Arg	Cys	Phe	Phe	His	
		115					120					125				

TCT	GTC	TGT	CCG	GCA	GGG	ATG	ATT	GTC	AAG	TTC	CCA	GGC	ACG	GCG	CAG	432
Ser	Val	Cys	Pro	Ala	Gly	Met	Ile	Val	Lys	Phe	Pro	Gly	Thr	Ala	Gln	
	130					135					140					
AAG	AAC	ACG	GTC	TGT	GAG	CCG	GCT	TCC	CCA	GGG	GTC	AGC	CCT	GCC	TGT	480
Lys	Asn	Thr	Val	Cys	Glu	Pro	Ala	Ser	Pro	Gly	Val	Ser	Pro	Ala	Cys	
	145				150					155					160	
GCC	AGC	CCA	GAG	AAC	TGC	AAG	GAA	CCC	TCC	AGT	GGC	ACC	ATC	CCC	CAG	528
Ala	Ser	Pro	Glu	Asn	Cys	Lys	Glu	Pro	Ser	Ser	Gly	Thr	Ile	Pro	Gln	
				165					170					175		
GCC	AAG	CCC	ACC	CCG	GTG	TCC	CCA	GCA	ACC	TCC	AGT	GCC	AGC	ACC	ATG	576
Ala	Lys	Pro	Thr	Pro	Val	Ser	Pro	Ala	Thr	Ser	Ser	Ala	Ser	Thr	Met	
			180					185						190		
CCT	GTA	AGA	GGG	GGC	ACC	CGC	CTC	GCC	CAG	GAA	GCT	GCT	TCT	AAA	CTG	624
Pro	Val	Arg	Gly	Gly	Thr	Arg	Leu	Ala	Gln	Glu	Ala	Ala	Ser	Lys	Leu	
		195					200					205				
ACG	AGG	GCT	CCC	GAC	TCT	CCC	TCC	TCT	GTG	GGA	AGG	CCT	AGT	TCA	GAT	672
Thr	Arg	Ala	Pro	Asp	Ser	Pro	Ser	Ser	Val	Gly	Arg	Pro	Ser	Ser	Asp	
	210					215					220					
CCA	GGT	CTG	TCC	CCA	ACA	CAG	CCA	TGC	CCA	GAG	GGG	TCT	GGT	GAT	TGC	720
Pro	Gly	Leu	Ser	Pro	Thr	Gln	Pro	Cys	Pro	Glu	Gly	Ser	Gly	Asp	Cys	
	225				230					235					240	
AGA	AAG	CAG	TGT	GAG	CCC	GAC	TAC	TAC	CTG	GAC	GAG	GCC	GGC	CGC	TGC	768
Arg	Lys	Gln	Cys	Glu	Pro	Asp	Tyr	Tyr	Leu	Asp	Glu	Ala	Gly	Arg	Cys	
				245					250					255		
ACA	GCC	TGC	GTG	AGC	TGT	TCT	CGA	GAT	GAC	CTT	GTG	GAG	AAG	ACG	CCA	816
Thr	Ala	Cys	Val	Ser	Cys	Ser	Arg	Asp	Asp	Leu	Val	Glu	Lys	Thr	Pro	
			260					265						270		
TGT	GCA	TGG	AAC	TCC	TCC	CGC	ACC	TGC	GAA	TGT	CGA	CCT	GGC	ATG	ATC	864
Cys	Ala	Trp	Asn	Ser	Ser	Arg	Thr	Cys	Glu	Cys	Arg	Pro	Gly	Met	Ile	
		275					280					285				
TGT	GCC	ACA	TCA	GCC	ACC	AAC	TCC	TGT	GCC	CGC	TGT	GTC	CCC	TAC	CCA	912
Cys	Ala	Thr	Ser	Ala	Thr	Asn	Ser	Cys	Ala	Arg	Cys	Val	Pro	Tyr	Pro	
	290					295					300					
ATC	TGT	GCA	GGA	GAG	ACG	GTC	ACC	AAG	CCC	CAG	GAT	ATG	GCT	GAG	AAG	960
Ile	Cys	Ala	Gly	Glu	Thr	Val	Thr	Lys	Pro	Gln	Asp	Met	Ala	Glu	Lys	
	305				310					315					320	
GAC	ACC	ACC	TTT	GAG	GCG	CCA	CCC	CTG	GGG	ACC	CAG	CCG	GAC	TGC	AAC	1008
Asp	Thr	Thr	Phe	Glu	Ala	Pro	Pro	Leu	Gly	Thr	Gln	Pro	Asp	Cys	Asn	
				325					330					335		
CCC	ACC	CCA	GAG	AAT	GGC	GAG	GCG	CCT	GCC	AGC	ACC	AGC	CCC	ACT	CAG	1056
Pro	Thr	Pro	Glu	Asn	Gly	Glu	Ala	Pro	Ala	Ser	Thr	Ser	Pro	Thr	Gln	
			340					345					350			
AGC	TTG	CTG	GTG	GAC	TCC	CAG	GCC	AGT	AAG	ACG	CTG	CCC	ATC	CCA	ACC	1104
Ser	Leu	Leu	Val	Asp	Ser	Gln	Ala	Ser	Lys	Thr	Leu	Pro	Ile	Pro	Thr	
		355					360					365				
AGC	GCT	CCC	GTC	GCT	CTC	TCC	TCC	ACG	GGG	AAG	CCC	GTT	CTG	GAT	GCA	1152

Ser	Ala	Pro	Val	Ala	Leu	Ser	Ser	Thr	Gly	Lys	Pro	Val	Leu	Asp	Ala		
370						375					380						
GGG	CCA	GTG	CTC	TTC	TGG	GTG	ATC	CTG	GTG	TTG	GTT	GTG	GTG	GTC	GGC	1200	
Gly	Pro	Val	Leu	Phe	Trp	Val	Ile	Leu	Val	Leu	Val	Val	Val	Val	Gly	400	
385					390					395							
TCC	AGC	GCC	TTC	CTC	CTG	TGC	CAC	CGG	AGG	GCC	TGC	AGG	AAG	CGA	ATT	1248	
Ser	Ser	Ala	Phe	Leu	Leu	Cys	His	Arg	Arg	Ala	Cys	Arg	Lys	Arg	Ile		
				405				410						415			
CGG	CAG	AAG	CTC	CAC	CTG	TGC	TAC	CCG	GTC	CAG	ACC	TCC	CAG	CCC	AAG	1296	
Arg	Gln	Lys	Leu	His	Leu	Cys	Tyr	Pro	Val	Gln	Thr	Ser	Gln	Pro	Lys		
			420					425					430				
CTA	GAG	CTT	GTG	GAT	TCC	AGA	CCC	AGG	AGG	AGC	TCA	ACG	CAG	CTG	AGG	1344	
Leu	Glu	Leu	Val	Asp	Ser	Arg	Pro	Arg	Arg	Ser	Ser	Thr	Gln	Leu	Arg		
			435				440					445					
AGT	GGT	GCG	TCG	GTG	ACA	GAA	CCC	GTC	GCG	GAA	GAG	CGA	GGG	TTA	ATG	1392	
Ser	Gly	Ala	Ser	Val	Thr		Pro	Val	Ala	Glu	Glu	Arg	Gly	Leu	Met		
450						455					460						
AGC	CAG	CCA	CTG	ATG	GAG	ACC	TGC	CAC	AGC	GTG	GGG	GCA	GCC	TAC	CTG	1440	
Ser	Gln	Pro	Leu	Met	Glu	Thr	Cys	His	Ser	Val	Gly	Ala	Ala	Tyr	Leu		
465					470					475					480		
GAG	AGC	CTG	CCG	CTG	CAG	GAT	GCC	AGC	CCG	GCC	GGG	GGC	CCC	TCG	TCC	1488	
Glu	Ser	Leu	Pro	Leu	Gln	Asp	Ala	Ser	Pro	Ala	Gly	Gly	Pro		Ser		
				485					490					495			
CCC	AGG	GAC	CTT	CCT	GAG	CCC	CGG	GTG	TCC	ACG	GAG	CAC	ACC	AAT	AAC	1536	
Pro	Arg	Asp	Leu	Pro	Glu	Pro	Arg	Val	Ser	Thr	Glu	His	Thr	Asn	Asn		
			500					505					510				
AAG	ATT	GAG	AAA	ATC	TAC	ATC	ATG	AAG	GCT	GAC	ACC	GTG	ATC	GTG	GGG	1584	
Lys	Ile	Glu	Lys	Ile	Tyr	Ile	Met	Lys	Ala	Asp	Thr	Val	Ile	Val	Gly		
			515					520				525					
ACC	GTG	AAG	GCT	GAG	CTG	CCG	GAG	GGC	CGG	GGC	CTG	GCG	GGG	CCA	GCA	1632	
Thr	Val	Lys	Ala	Glu	Leu	Pro	Glu	Gly	Arg	Gly	Leu	Ala	Gly	Pro	Ala		
			530				535				540						
GAG	CCC	GAG	TTG	GAG	GAG	GAG	CTG	GAG	GCG	GAC	CAT	ACC	CCC	CAC	TAC	1680	
Glu	Pro	Glu	Leu	Glu	Glu	Glu	Leu	Glu	Ala	Asp	His	Thr	Pro	His	Tyr		
545					550					555					560		
CCC	GAG	CAG	GAG	ACA	GAA	CCG	CCT	CTG	GGC	AGC	TGC	AGC	GAT	GTC	ATG	1728	
Pro	Glu	Gln	Glu	Thr	Glu	Pro	Pro	Leu	Gly	Ser	Cys	Ser	Asp	Val	Met		
				565					570					575			
CTC	TCA	GTG	GAA	GAG	GAA	GGG	AAA	GAA	GAC	CCC	TTG	CCC	ACA	GCT	GCC	1776	
Leu	Ser	Val	Glu	Glu	Glu	Gly	Lys	Glu	Asp	Pro	Leu	Pro	Thr	Ala	Ala		
			580					585					590				
TCT	GGA	AAG	TGA													1788	
Ser	Gly	Lys															
			595														

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 595 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Arg	Val	Leu	Leu	Ala	Ala	Leu	Gly	Leu	Leu	Phe	Leu	Gly	Ala	Leu	
1				5					10					15		
Arg	Ala	Phe	Pro	Gln	Asp	Arg	Pro	Phe	Glu	Asp	Thr	Cys	His	Gly	Asn	
			20					25					30			
Pro	Ser	His	Tyr	Tyr	Asp	Lys	Ala	Val	Arg	Arg	Cys	Cys	Tyr	Arg	Cys	
		35					40					45				
Pro	Met	Gly	Leu	Phe	Pro	Thr	Gln	Gln	Cys	Pro	Gln	Arg	Pro	Thr	Asp	
	50					55					60					
Cys	Arg	Lys	Gln	Cys	Glu	Pro	Asp	Tyr	Tyr	Leu	Asp	Glu	Ala	Asp	Arg	
65					70					75					80	
Cys	Thr	Ala	Cys	Val	Thr	Cys	Ser	Arg	Asp	Asp	Leu	Val	Glu	Lys	Thr	
				85					90					95		
Pro	Cys	Ala	Trp	Asn	Ser	Ser	Arg	Val	Cys	Glu	Cys	Arg	Pro	Gly	Met	
			100					105					110			
Phe	Cys	Ser	Thr	Ser	Ala	Val	Asn	Ser	Cys	Ala	Arg	Cys	Phe	Phe	His	
		115					120					125				
Ser	Val	Cys	Pro	Ala	Gly	Met	Ile	Val	Lys	Phe	Pro	Gly	Thr	Ala	Gln	
	130					135					140					
Lys	Asn	Thr	Val	Cys	Glu	Pro	Ala	Ser	Pro	Gly	Val	Ser	Pro	Ala	Cys	
145					150					155					160	
Ala	Ser	Pro	Glu	Asn	Cys	Lys	Glu	Pro	Ser	Ser	Gly	Thr	Ile	Pro	Gln	
				165					170					175		
Ala	Lys	Pro	Thr	Pro	Val	Ser	Pro	Ala	Thr	Ser	Ser	Ala	Ser	Thr	Met	
			180					185					190			
Pro	Val	Arg	Gly	Gly	Thr	Arg	Leu	Ala	Gln	Glu	Ala	Ala	Ser	Lys	Leu	
		195					200					205				
Thr	Arg	Ala	Pro	Asp	Ser	Pro	Ser	Ser	Val	Gly	Arg	Pro	Ser	Ser	Asp	
	210					215					220					
Pro	Gly	Leu	Ser	Pro	Thr	Gln	Pro	Cys	Pro	Glu	Gly	Ser	Gly	Asp	Cys	
225					230					235					240	
Arg	Lys	Gln	Cys	Glu	Pro	Asp	Tyr	Tyr	Leu	Asp	Glu	Ala	Gly	Arg	Cys	
				245					250					255		
Thr	Ala	Cys	Val	Ser	Cys	Ser	Arg	Asp	Asp	Leu	Val	Glu	Lys	Thr	Pro	
			260					265					270			

Cys Ala Trp Asn Ser Ser Arg Thr Cys Glu Cys Arg Pro Gly Met Ile
 275 280 285
 Cys Ala Thr Ser Ala Thr Asn Ser Cys Ala Arg Cys Val Pro Tyr Pro
 290 295 300
 Ile Cys Ala Gly Glu Thr Val Thr Lys Pro Gln Asp Met Ala Glu Lys
 305 310 315 320
 Asp Thr Thr Phe Glu Ala Pro Pro Leu Gly Thr Gln Pro Asp Cys Asn
 325 330 335
 Pro Thr Pro Glu Asn Gly Glu Ala Pro Ala Ser Thr Ser Pro Thr Gln
 340 345 350
 Ser Leu Leu Val Asp Ser Gln Ala Ser Lys Thr Leu Pro Ile Pro Thr
 355 360 365
 Ser Ala Pro Val Ala Leu Ser Ser Thr Gly Lys Pro Val Leu Asp Ala
 370 375 380
 Gly Pro Val Leu Phe Trp Val Ile Leu Val Leu Val Val Val Gly
 385 390 395 400
 Ser Ser Ala Phe Leu Leu Cys His Arg Arg Ala Cys Arg Lys Arg Ile
 405 410 415
 Arg Gln Lys Leu His Leu Cys Tyr Pro Val Gln Thr Ser Gln Pro Lys
 420 425 430
 Leu Glu Leu Val Asp Ser Arg Pro Arg Arg Ser Ser Thr Gln Leu Arg
 435 440 445
 Ser Gly Ala Ser Val Thr Glu Pro Val Ala Glu Glu Arg Gly Leu Met
 450 455 460
 Ser Gln Pro Leu Met Glu Thr Cys His Ser Val Gly Ala Ala Tyr Leu
 465 470 475 480
 Glu Ser Leu Pro Leu Gln Asp Ala Ser Pro Ala Gly Gly Pro Ser Ser
 485 490 495
 Pro Arg Asp Leu Pro Glu Pro Arg Val Ser Thr Glu His Thr Asn Asn
 500 505 510
 Lys Ile Glu Lys Ile Tyr Ile Met Lys Ala Asp Thr Val Ile Val Gly
 515 520 525
 Thr Val Lys Ala Glu Leu Pro Glu Gly Arg Gly Leu Ala Gly Pro Ala
 530 535 540
 Glu Pro Glu Leu Glu Glu Glu Leu Glu Ala Asp His Thr Pro His Tyr
 545 550 555 560
 Pro Glu Gln Glu Thr Glu Pro Pro Leu Gly Ser Cys Ser Asp Val Met
 565 570 575
 Leu Ser Val Glu Glu Glu Gly Lys Glu Asp Pro Leu Pro Thr Ala Ala
 580 585 590
 Ser Gly Lys

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: hIgG1Fc

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAG	CCC	AGA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	CCG	TGC	CCA	GCA	48
Glu	Pro	Arg	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	
1				5					10					15		
CCT	GAA	CTC	CTG	GGG	GGA	CCG	TCA	GTC	TTC	CTC	TTC	CCC	CCA	AAA	CCC	96
Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	
			20					25					30			
AAG	GAC	ACC	CTC	ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACA	TGC	GTG	GTG	144
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	
		35					40					45				
GTG	GAC	GTG	AGC	CAC	GAA	GAC	CCT	GAG	GTC	AAG	TTC	AAC	TGG	TAC	GTG	192
Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	
	50					55				60						
GAC	GGC	GTG	GAG	GTG	CAT	AAT	GCC	AAG	ACA	AAG	CCG	CGG	GAG	GAG	CAG	240
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	
65					70				75						80	
TAC	AAC	AGC	ACG	TAC	CGG	GTG	GTC	AGC	GTC	CTC	ACC	GTC	CTG	CAC	CAG	288
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	
			85					90						95		
GAC	TGG	CTG	AAT	GGC	AAG	GAC	TAC	AAG	TGC	AAG	GTC	TCC	AAC	AAA	GCC	336
Asp	Trp	Leu	Asn	Gly	Lys	Asp	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	
		100						105					110			
CTC	CCA	GCC	CCC	ATG	CAG	AAA	ACC	ATC	TCC	AAA	GCC	AAA	GGG	CAG	CCC	384
Leu	Pro	Ala	Pro	Met	Gln	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	
		115					120					125				
CGA	GAA	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CGG	GAT	GAG	CTG	ACC	432

Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr		
130						135					140						
AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GGC	TTC	TAT	CCC	AGG	480	
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Arg	160	
145					150					155							
CAC	ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	CAG	CCG	GAG	AAC	AAC	TAC	528	
His	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	175	
				165					170								
AAG	ACC	ACG	CCT	CCC	GTG	CTG	GAC	TCC	GAC	GGC	TCC	TTC	TTC	CTC	TAC	576	
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	190	
			180					185									
AGC	AAG	CTC	ACC	GTG	GAC	AAG	AGC	AGG	TGG	CAG	CAG	GGG	AAC	GTC	TTC	624	
Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	205	
		195					200					205					
TCA	TGC	TCC	GTG	ATG	CAT	GAG	GCT	CTG	CAC	AAC	CAC	TAC	ACG	CAG	AAG	672	
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	220	
	210					215					220						
AGC	CTC	TCC	CTG	TCT	CCG	GGT	AAA	TGA								699	
Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys										
225						230											

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu	Pro	Arg	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala		
1				5					10					15			
Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro		
		20					25					30					
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val		
	35						40					45					
Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val		
	50					55					60						
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln		
65					70					75					80		
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln		
			85						90					95			
Asp	Trp	Leu	Asn	Gly	Lys	Asp	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala		
		100						105					110				
Leu	Pro	Ala	Pro	Met	Gln	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro		

115					120					125					
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr
130						135					140				
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Arg
145					150					155					160
His	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr
				165					170					175	
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr
			180					185					190		
Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe
		195					200					205			
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys
210						215					220				
Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys								
225					230										

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 720 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: muCD30-L
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..720
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG	GAG	CCA	GGG	CTG	CAA	CAA	GCA	GGC	AGC	TGT	GGG	GCT	CCT	TCC	CCT	48
Met	Glu	Pro	Gly	Leu	Gln	Gln	Ala	Gly	Ser	Cys	Gly	Ala	Pro	Ser	Pro	
1				5				10						15		
GAC	CCA	GCC	ATG	CAG	GTG	CAG	CCC	GGC	TCG	GTA	GCC	AGC	CCC	TGG	AGA	96
Asp	Pro	Ala	Met	Gln	Val	Gln	Pro	Gly	Ser	Val	Ala	Ser	Pro	Trp	Arg	
			20					25					30			
AGC	ACG	AGG	CCC	TGG	AGA	AGC	ACA	AGT	CGC	AGC	TAC	TTC	TAC	CTC	AGC	144
Ser	Thr	Arg	Pro	Trp	Arg	Ser	Thr	Ser	Arg	Ser	Tyr	Phe	Tyr	Leu	Ser	
			35				40					45				
ACC	ACC	GCA	CTG	GTG	TGC	CTT	GTT	GTG	GCA	GTG	GCG	ATC	ATT	CTG	GTA	192
Thr	Thr	Ala	Leu	Val	Cys	Leu	Val	Val	Ala	Val	Ala	Ile	Ile	Leu	Val	

50	55	60	
CTG GTA GTC CAG AAA AAG GAC TCC ACT CCA AAT ACA ACT GAG AAG GCC			240
Leu Val Val Gln Lys Lys Asp Ser Thr Pro Asn Thr Thr Glu Lys Ala			
65	70	75	80
CCC CTT AAA GGA GGA AAT TGC TCA GAG GAT CTC TTC TGT ACC CTG AAA			288
Pro Leu Lys Gly Gly Asn Cys Ser Glu Asp Leu Phe Cys Thr Leu Lys			
	85	90	95
AGT ACT CCA TCC AAG AAG TCA TGG GCC TAC CTC CAA GTG TCA AAG CAT			336
Ser Thr Pro Ser Lys Lys Ser Trp Ala Tyr Leu Gln Val Ser Lys His			
	100	105	110
CTC AAC AAT ACC AAA CTG TCA TGG AAC GAA GAT GGC ACC ATC CAC GGA			384
Leu Asn Asn Thr Lys Leu Ser Trp Asn Glu Asp Gly Thr Ile His Gly			
	115	120	125
CTC ATA TAC CAG GAC GGG AAC CTG ATA GTC CAA TTC CCT GGC TTG TAC			432
Leu Ile Tyr Gln Asp Gly Asn Leu Ile Val Gln Phe Pro Gly Leu Tyr			
	130	135	140
TTC ATC GTT TGC CAA CTG CAG TTC CTC GTG CAG TGC TCA AAT CAT TCT			480
Phe Ile Val Cys Gln Leu Gln Phe Leu Val Gln Cys Ser Asn His Ser			
	145	150	155
GTG GAC CTG ACA TTG CAG CTC CTC ATC AAT TCC AAG ATC AAA AAG CAG			528
Val Asp Leu Thr Leu Gln Leu Leu Ile Asn Ser Lys Ile Lys Lys Gln			
	165	170	175
ACG TTG GTA ACA GTG TGT GAG TCT GGA GTT CAG AGT AAG AAC ATC TAC			576
Thr Leu Val Thr Val Cys Glu Ser Gly Val Gln Ser Lys Asn Ile Tyr			
	180	185	190
CAG AAT CTC TCT CAG TTT TTG CTG CAT TAC TTA CAG GTC AAC TCT ACC			624
Gln Asn Leu Ser Gln Phe Leu Leu His Tyr Leu Gln Val Asn Ser Thr			
	195	200	205
ATA TCA GTC AGG GTG GAT AAT TTC CAG TAT GTG GAT ACA AAC ACT TTC			672
Ile Ser Val Arg Val Asp Asn Phe Gln Tyr Val Asp Thr Asn Thr Phe			
	210	215	220
CCT CTT GAT AAT GTG CTA TCC GTC TTC TTA TAT AGT AGC TCA GAC TGA			720
Pro Leu Asp Asn Val Leu Ser Val Phe Leu Tyr Ser Ser Ser Asp			
	225	230	235
			240

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Glu	Pro	Gly	Leu	Gln	Gln	Ala	Gly	Ser	Cys	Gly	Ala	Pro	Ser	Pro
1				5				10					15		

Asp Pro Ala Met Gln Val Gln Pro Gly Ser Val Ala Ser Pro Trp Arg
 20 25 30
 Ser Thr Arg Pro Trp Arg Ser Thr Ser Arg Ser Tyr Phe Tyr Leu Ser
 35 40 45
 Thr Thr Ala Leu Val Cys Leu Val Val Ala Val Ala Ile Ile Leu Val
 50 55 60
 Leu Val Val Gln Lys Lys Asp Ser Thr Pro Asn Thr Thr Glu Lys Ala
 65 70 75 80
 Pro Leu Lys Gly Gly Asn Cys Ser Glu Asp Leu Phe Cys Thr Leu Lys
 85 90 95
 Ser Thr Pro Ser Lys Lys Ser Trp Ala Tyr Leu Gln Val Ser Lys His
 100 105 110
 Leu Asn Asn Thr Lys Leu Ser Trp Asn Glu Asp Gly Thr Ile His Gly
 115 120 125
 Leu Ile Tyr Gln Asp Gly Asn Leu Ile Val Gln Phe Pro Gly Leu Tyr
 130 135 140
 Phe Ile Val Cys Gln Leu Gln Phe Leu Val Gln Cys Ser Asn His Ser
 145 150 155 160
 Val Asp Leu Thr Leu Gln Leu Leu Ile Asn Ser Lys Ile Lys Lys Gln
 165 170 175
 Thr Leu Val Thr Val Cys Glu Ser Gly Val Gln Ser Lys Asn Ile Tyr
 180 185 190
 Gln Asn Leu Ser Gln Phe Leu Leu His Tyr Leu Gln Val Asn Ser Thr
 195 200 205
 Ile Ser Val Arg Val Asp Asn Phe Gln Tyr Val Asp Thr Asn Thr Phe
 210 215 220
 Pro Leu Asp Asn Val Leu Ser Val Phe Leu Tyr Ser Ser Ser Asp
 225 230 235

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: huCD30-L

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG GAC CCA GGG CTG CAG CAA GCA CTC AAC GGA ATG GCC CCT CCT GGA	48
Met Asp Pro Gly Leu Gln Gln Ala Leu Asn Gly Met Ala Pro Pro Gly	
1 5 10 15	
GAC ACA GCC ATG CAT GTG CCG GCG GGC TCC GTG GCC AGC CAC CTG GGG	96
Asp Thr Ala Met His Val Pro Ala Gly Ser Val Ala Ser His Leu Gly	
20 25 30	
ACC ACG AGC CGC AGC TAT TTC TAT TTG ACC ACA GCC ACT CTG GCT CTG	144
Thr Thr Ser Arg Ser Tyr Phe Tyr Leu Thr Thr Ala Thr Leu Ala Leu	
35 40 45	
TGC CTT GTC TTC ACG GTG GCC ACT ATT ATG GTG TTG GTC GTT CAG AGG	192
Cys Leu Val Phe Thr Val Ala Thr Ile Met Val Leu Val Val Gln Arg	
50 55 60	
ACG GAC TCC ATT CCC AAC TCA CCT GAC AAC GTC CCC CTC AAA GGA GGA	240
Thr Asp Ser Ile Pro Asn Ser Pro Asp Asn Val Pro Leu Lys Gly Gly	
65 70 75 80	
AAT TGC TCA GAA GAC CTC TTA TGT ATC CTG AAA AGA GCT CCA TTC AAG	288
Asn Cys Ser Glu Asp Leu Leu Cys Ile Leu Lys Arg Ala Pro Phe Lys	
85 90 95	
AAG TCA TGG GCC TAC CTC CAA GTG GCA AAG CAT CTA AAC AAA ACC AAG	336
Lys Ser Trp Ala Tyr Leu Gln Val Ala Lys His Leu Asn Lys Thr Lys	
100 105 110	
TTG TCT TGG AAC AAA GAT GGC ATT CTC CAT GGA GTC AGA TAT CAG GAT	384
Leu Ser Trp Asn Lys Asp Gly Ile Leu His Gly Val Arg Tyr Gln Asp	
115 120 125	
GGG AAT CTG GTG ATC CAA TTC CCT GGT TTG TAC TTC ATC ATT TGC CAA	432
Gly Asn Leu Val Ile Gln Phe Pro Gly Leu Tyr Phe Ile Ile Cys Gln	
130 135 140	
CTG CAG TTT CTT GTA CAA TGC CCA AAT AAT TCT GTC GAT CTG AAG TTG	480
Leu Gln Phe Leu Val Gln Cys Pro Asn Asn Ser Val Asp Leu Lys Leu	
145 150 155 160	
GAG CTT CTC ATC AAC AAG CAT ATC AAA AAA CAG GCC CTG GTG ACA GTG	528
Glu Leu Leu Ile Asn Lys His Ile Lys Lys Gln Ala Leu Val Thr Val	
165 170 175	
TGT GAG TCT GGA ATG CAA ACG AAA CAC GTA TAC CAG AAT CTC TCT CAA	576
Cys Glu Ser Gly Met Gln Thr Lys His Val Tyr Gln Asn Leu Ser Gln	
180 185 190	
TTC TTG CTG GAT TAC CTG CAG GTC AAC ACC ACC ATA TCA GTC AAT GTG	624
Phe Leu Leu Asp Tyr Leu Gln Val Asn Thr Thr Ile Ser Val Asn Val	
195 200 205	
GAT ACA TTC CAG TAC ATA GAT ACA AGC ACC TTT CCT CTT GAG AAT GTG	672
Asp Thr Phe Gln Tyr Ile Asp Thr Ser Thr Phe Pro Leu Glu Asn Val	
210 215 220	
TTG TCC ATC TTC TTA TAC AGT AAT TCA GAC TGA	705
Leu Ser Ile Phe Leu Tyr Ser Asn Ser Asp	

235

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

(2) INFORMATION FOR SEO ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:
 (B) CLONE: 5' PCR Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATAGCGGCCG CCACCATGCG CGTCCTCCTC GCCGCGCTG 39

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:
 (B) CLONE: 3' PCR Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ACAAGATCTG GGCTCCTTCC CCGTGGAGGA GAGAGCGAC 39

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:
 (B) CLONE: BGL II Adaptor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GATCTGGCAA CGAAGGTACC ATGG 24

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:
 (B) CLONE: BGL II Adaptor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCATGGTACC TTCGTTGCCA 20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
 (B) CLONE: Upstream sequence

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATG	GGC	TGT	GGG	GCT	CCT	TCC	CCT	GAC	CCA	GCC	33
Met	Gly	Cys	Gly	Ala	Pro	Ser	Pro	Asp	Pro	Ala	
1				5						10	

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Gly	Cys	Gly	Ala	Pro	Ser	Pro	Asp	Pro	Ala
1				5						10

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
 (B) CLONE: FLAG peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:
 (B) CLONE: Murine cDNA Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AGATGCTTTG ACACTTG 17

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:
 (B) CLONE: Human cDNA Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATCACCAGAT TCCCATC 17

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 663 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: muCD30-L

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATG CAG GTG CAG CCC GGC TCG GTA GCC AGC CCC TGG AGA AGC ACG AGG	48
Met Gln Val Gln Pro Gly Ser Val Ala Ser Pro Trp Arg Ser Thr Arg	
1 5 10 15	
CCC TGG AGA AGC ACA AGT CGC AGC TAC TTC TAC CTC AGC ACC ACC GCA	96
Pro Trp Arg Ser Thr Ser Arg Ser Tyr Phe Tyr Leu Ser Thr Thr Ala	
20 25 30	
CTG GTG TGC CTT GTT GTG GCA GTG GCG ATC ATT CTG GTA CTG GTA GTC	144
Leu Val Cys Leu Val Val Ala Val Ala Ile Ile Leu Val Leu Val Val	
35 40 45	
CAG AAA AAG GAC TCC ACT CCA AAT ACA ACT GAG AAG GCC CCC CTT AAA	192
Gln Lys Lys Asp Ser Thr Pro Asn Thr Thr Glu Lys Ala Pro Leu Lys	
50 55 60	
GGA GGA AAT TGC TCA GAG GAT CTC TTC TGT ACC CTG AAA AGT ACT CCA	240
Gly Gly Asn Cys Ser Glu Asp Leu Phe Cys Thr Leu Lys Ser Thr Pro	
65 70 75 80	
TCC AAG AAG TCA TGG GCC TAC CTC CAA GTG TCA AAG CAT CTC AAC AAT	288
Ser Lys Lys Ser Trp Ala Tyr Leu Gln Val Ser Lys His Leu Asn Asn	
85 90 95	
ACC AAA CTG TCA TGG AAC GAA GAT GGC ACC ATC CAC GGA CTC ATA TAC	336
Thr Lys Leu Ser Trp Asn Glu Asp Gly Thr Ile His Gly Leu Ile Tyr	
100 105 110	
CAG GAC GGG AAC CTG ATA GTC CAA TTC CCT GGC TTG TAC TTC ATC GTT	384
Gln Asp Gly Asn Leu Ile Val Gln Phe Pro Gly Leu Tyr Phe Ile Val	
115 120 125	
TGC CAA CTG CAG TTC CTC GTG CAG TGC TCA AAT CAT TCT GTG GAC CTG	432
Cys Gln Leu Gln Phe Leu Val Gln Cys Ser Asn His Ser Val Asp Leu	
130 135 140	
ACA TTG CAG CTC CTC ATC AAT TCC AAG ATC AAA AAG CAG ACG TTG GTA	480
Thr Leu Gln Leu Leu Ile Asn Ser Lys Ile Lys Lys Gln Thr Leu Val	
145 150 155 160	

ACA GTG TGT GAG TCT GGA GTT CAG AGT AAG AAC ATC TAC CAG AAT CTC	528
Thr Val Cys Glu Ser Gly Val Gln Ser Lys Asn Ile Tyr Gln Asn Leu	
165 170 175	
TCT CAG TTT TTG CTG CAT TAC TTA CAG GTC AAC TCT ACC ATA TCA GTC	576
Ser Gln Phe Leu Leu His Tyr Leu Gln Val Asn Ser Thr Ile Ser Val	
180 185 190	
AGG GTG GAT AAT TTC CAG TAT GTG GAT ACA AAC ACT TTC CCT CTT GAT	624
Arg Val Asp Asn Phe Gln Tyr Val Asp Thr Asn Thr Phe Pro Leu Asp	
195 200 205	
AAT GTG CTA TCC GTC TTC TTA TAT AGT AGC TCA GAC TGA	663
Asn Val Leu Ser Val Phe Leu Tyr Ser Ser Ser Asp	
210 215 220	

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Gln Val Gln Pro Gly Ser Val Ala Ser Pro Trp Arg Ser Thr Arg	
1 5 10 15	
Pro Trp Arg Ser Thr Ser Arg Ser Tyr Phe Tyr Leu Ser Thr Thr Ala	
20 25 30	
Leu Val Cys Leu Val Val Ala Val Ala Ile Ile Leu Val Leu Val Val	
35 40 45	
Gln Lys Lys Asp Ser Thr Pro Asn Thr Thr Glu Lys Ala Pro Leu Lys	
50 55 60	
Gly Gly Asn Cys Ser Glu Asp Leu Phe Cys Thr Leu Lys Ser Thr Pro	
65 70 75 80	
Ser Lys Lys Ser Trp Ala Tyr Leu Gln Val Ser Lys His Leu Asn Asn	
85 90 95	
Thr Lys Leu Ser Trp Asn Glu Asp Gly Thr Ile His Gly Leu Ile Tyr	
100 105 110	
Gln Asp Gly Asn Leu Ile Val Gln Phe Pro Gly Leu Tyr Phe Ile Val	
115 120 125	
Cys Gln Leu Gln Phe Leu Val Gln Cys Ser Asn His Ser Val Asp Leu	
130 135 140	
Thr Leu Gln Leu Leu Ile Asn Ser Lys Ile Lys Lys Gln Thr Leu Val	
145 150 155 160	
Thr Val Cys Glu Ser Gly Val Gln Ser Lys Asn Ile Tyr Gln Asn Leu	
165 170 175	

Ser Gln Phe Leu Leu His Tyr Leu Gln Val Asn Ser Thr Ile Ser Val
180 185 190

Arg Val Asp Asn Phe Gln Tyr Val Asp Thr Asn Thr Phe Pro Leu Asp
195 200 205

Asn Val Leu Ser Val Phe Leu Tyr Ser Ser Ser Asp
210 215 220

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein fragment

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: huCD30-L fragment (PRELIM)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Pro Gly Asp Thr Val Xaa His Val Pro Ala Gly Ser Glu Ala Ser His
1 5 10 15

Leu Gly Thr Thr Ser Arg Xaa Tyr Phe Tyr Leu Thr Thr Xaa Thr Leu
20 25 30

Ala Leu Cys Leu Val Phe Thr Val Ala Thr Ile Met Val Leu Val Val
35 40 45

Gln Arg Thr Asp Ser Ile Pro Asn Ser Pro Asp Asn Val Pro Leu Lys
50 55 60

Gly Gly Asn Cys Ser Glu Asp Leu Leu Cys Ile Leu Lys Arg Ala Pro
65 70 75 80

Phe Lys Lys Ser Trp Ala Tyr Leu Gln Val Xaa Lys His Leu Asn Lys
85 90 95

Thr Xaa Leu Ser Trp Asn Lys Asp Gly Ile Leu His Gly Val Arg Tyr
100 105 110

Gln Asp Gly Asn Leu Val Ile Gln Phe Pro Gly Phe Val
115 120 125

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein fragment
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: muCD30-L fragment (PRELIM)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

Met Gln Val Gln Pro Gly Ser Val Ala Ser Pro Trp Arg Ser Thr Arg
1      5      10      15
Pro Trp Arg Ser Thr Ser Arg Ser Tyr Phe Tyr Leu Ser Thr Thr Ala
20      25      30
Leu Val Cys Leu Val Val Xaa Val Ala Ile Ile Leu Val Leu Val Val
35      40      45
Gln Lys Lys Asp Ser Thr Pro Asn Thr Thr Glu Lys Ala Pro Leu Lys
50      55      60
Gly Gly Asn Cys Ser Glu Asp Leu Phe Cys Thr Leu Lys Ser Thr Pro
65      70      75      80
Ser Lys Lys Ser Trp Ala Tyr Leu Gln Val Ser Lys His Leu Asn Asn
85      90      95
Thr Lys Leu Ser Trp Asn Glu Asp Gly Thr Ile His Gly Leu Ile Tyr
100     105     110
Gln Asp Gly Asn Leu Ile Val Gln Phe Pro Gly Leu Tyr Phe Ile Val
115     120     125
Cys Gln
130

```

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 648 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: huCD30-L
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..648
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATG	CAT	GTG	CCG	GCG	GGC	TCC	GTG	GCC	AGC	CAC	CTG	GGG	ACC	ACG	AGC	48
Met	His	Val	Pro	Ala	Gly	Ser	Val	Ala	Ser	His	Leu	Gly	Thr	Thr	Ser	
1				5					10					15		
CGC	AGC	TAT	TTC	TAT	TTG	ACC	ACA	GCC	ACT	CTG	GCT	CTG	TGC	CTT	GTC	96
Arg	Ser	Tyr	Phe	Tyr	Leu	Thr	Thr	Ala	Thr	Leu	Ala	Leu	Cys	Leu	Val	
			20					25					30			
TTC	ACG	GTG	GCC	ACT	ATT	ATG	GTG	TTG	GTC	GTT	CAG	AGG	ACG	GAC	TCC	144
Phe	Thr	Val	Ala	Thr	Ile	Met	Val	Leu	Val	Val	Gln	Arg	Thr	Asp	Ser	
		35					40					45				
ATT	CCC	AAC	TCA	CCT	GAC	AAC	GTC	CCC	CTC	AAA	GGA	GGA	AAT	TGC	TCA	192
Ile	Pro	Asn	Ser	Pro	Asp	Asn	Val	Pro	Leu	Lys	Gly	Gly	Asn	Cys	Ser	
	50					55					60					
GAA	GAC	CTC	TTA	TGT	ATC	CTG	AAA	AGA	GCT	CCA	TTC	AAG	AAG	TCA	TGG	240
Glu	Asp	Leu	Leu	Cys	Ile	Leu	Lys	Arg	Ala	Pro	Phe	Lys	Lys	Ser	Trp	
65					70				75						80	
GCC	TAC	CTC	CAA	GTG	GCA	AAG	CAT	CTA	AAC	AAA	ACC	AAG	TTG	TCT	TGG	288
Ala	Tyr	Leu	Gln	Val	Ala	Lys	His	Leu	Asn	Lys	Thr	Lys	Leu	Ser	Trp	
			85					90						95		
AAC	AAA	GAT	GGC	ATT	CTC	CAT	GGA	GTC	AGA	TAT	CAG	GAT	GGG	AAT	CTG	336
Asn	Lys	Asp	Gly	Ile	Leu	His	Gly	Val	Arg	Tyr	Gln	Asp	Gly	Asn	Leu	
			100				105						110			
GTG	ATC	CAA	TTC	CCT	GGT	TTG	TAC	TTC	ATC	ATT	TGC	CAA	CTG	CAG	TTT	384
Val	Ile	Gln	Phe	Pro	Gly	Leu	Tyr	Phe	Ile	Ile	Cys	Gln	Leu	Gln	Phe	
		115					120					125				
CTT	GTA	CAA	TGC	CCA	AAT	AAT	TCT	GTC	GAT	CTG	AAG	TTG	GAG	CTT	CTC	432
Leu	Val	Gln	Cys	Pro	Asn	Asn	Ser	Val	Asp	Leu	Lys	Leu	Glu	Leu	Leu	
	130					135					140					
ATC	AAC	AAG	CAT	ATC	AAA	AAA	CAG	GCC	CTG	GTG	ACA	GTG	TGT	GAG	TCT	480
Ile	Asn	Lys	His	Ile	Lys	Lys	Gln	Ala	Leu	Val	Thr	Val	Cys	Glu	Ser	
145					150				155					160		
GGA	ATG	CAA	ACG	AAA	CAC	GTA	TAC	CAG	AAT	CTC	TCT	CAA	TTC	TTG	CTG	528
Gly	Met	Gln	Thr	Lys	His	Val	Tyr	Gln	Asn	Leu	Ser	Gln	Phe	Leu	Leu	
				165				170						175		
GAT	TAC	CTG	CAG	GTC	AAC	ACC	ACC	ATA	TCA	GTC	AAT	GTG	GAT	ACA	TTC	576
Asp	Tyr	Leu	Gln	Val	Asn	Thr	Thr	Ile	Ser	Val	Asn	Val	Asp	Thr	Phe	
			180					185					190			
CAG	TAC	ATA	GAT	ACA	AGC	ACC	TTT	CCT	CTT	GAG	AAT	GTG	TTG	TCC	ATC	624
Gln	Tyr	Ile	Asp	Thr	Ser	Thr	Phe	Pro	Leu	Glu	Asn	Val	Leu	Ser	Ile	
		195					200					205				
TTC	TTA	TAC	AGT	AAT	TCA	GAC	TGA									648
Phe	Leu	Tyr	Ser	Asn	Ser	Asp										
	210					215										

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met	His	Val	Pro	Ala	Gly	Ser	Val	Ala	Ser	His	Leu	Gly	Thr	Thr	Ser	1	5	10	15
Arg	Ser	Tyr	Phe	Tyr	Leu	Thr	Thr	Ala	Thr	Leu	Ala	Leu	Cys	Leu	Val	20	25	30	
Phe	Thr	Val	Ala	Thr	Ile	Met	Val	Leu	Val	Val	Gln	Arg	Thr	Asp	Ser	35	40	45	
Ile	Pro	Asn	Ser	Pro	Asp	Asn	Val	Pro	Leu	Lys	Gly	Gly	Asn	Cys	Ser	50	55	60	
Glu	Asp	Leu	Leu	Cys	Ile	Leu	Lys	Arg	Ala	Pro	Phe	Lys	Lys	Ser	Trp	65	70	75	80
Ala	Tyr	Leu	Gln	Val	Ala	Lys	His	Leu	Asn	Lys	Thr	Lys	Leu	Ser	Trp	85	90	95	
Asn	Lys	Asp	Gly	Ile	Leu	His	Gly	Val	Arg	Tyr	Gln	Asp	Gly	Asn	Leu	100	105	110	
Val	Ile	Gln	Phe	Pro	Gly	Leu	Tyr	Phe	Ile	Ile	Cys	Gln	Leu	Gln	Phe	115	120	125	
Leu	Val	Gln	Cys	Pro	Asn	Asn	Ser	Val	Asp	Leu	Lys	Leu	Glu	Leu	Leu	130	135	140	
Ile	Asn	Lys	His	Ile	Lys	Lys	Gln	Ala	Leu	Val	Thr	Val	Cys	Glu	Ser	145	150	155	160
Gly	Met	Gln	Thr	Lys	His	Val	Tyr	Gln	Asn	Leu	Ser	Gln	Phe	Leu	Leu	165	170	175	
Asp	Tyr	Leu	Gln	Val	Asn	Thr	Thr	Ile	Ser	Val	Asn	Val	Asp	Thr	Phe	180	185	190	
Gln	Tyr	Ile	Asp	Thr	Ser	Thr	Phe	Pro	Leu	Glu	Asn	Val	Leu	Ser	Ile	195	200	205	
Phe	Leu	Tyr	Ser	Asn	Ser	Asp	210	215											